

SEQUENCE LISTING



<110> HEINEGARD, DICK
LORENZO, PILAR

<120> CARTILAGE INTERMEDIATE LAYER PROTEIN AND NUCLEIC ACIDS
THEREFOR

<130> 02386.0046 SEQUENCE LISTING

<140> 09/609,383

<141> 2000-07-03

<150> 60/142,054

<151> 1999-07-02

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 4175

<212> DNA

<213> Homo sapiens

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MAR 15 2001
TECH CENTER 1600/2900

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 <213> Homo sapiens

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 35 40 45
 Thr Leu Glu Ser Pro Gly Glu Trp Thr Thr Leu Phe Asn Ile Asp Tyr
 50 55 60
 Pro Gly Gly Lys Gly Asp Tyr Glu Arg Leu Asp Ala Ile Arg Phe Tyr
 65 70 75 80
 Tyr Gly Asp Arg Val Cys Ala Arg Pro Leu Arg Leu Glu Ala Arg Thr
 85 90 95
 Thr Asp Trp Thr Pro Ala Gly Ser Thr Gly Gln Val Val His Gly Ser
 100 105 110
 Pro Arg Glu Gly Phe Trp Cys Leu Asn Arg Glu Gln Arg Pro Gly Gln
 115 120 125
 Asn Cys Ser Asn Tyr Thr Val Arg Phe Leu Cys Pro Pro Gly Ser Leu
 130 135 140
 Arg Arg Asp Thr Glu Arg Ile Trp Ser Pro Trp Ser Pro Trp Ser Lys
 145 150 155 160
 Cys Ser Ala Ala Cys Gly Gln Thr Gly Val Gln Thr Arg Thr Arg Ile
 165 170 175
 Cys Leu Ala Glu Met Val Ser Leu Cys Ser Glu Ala Ser Glu Glu Gly
 180 185 190
 Gln His Cys Met Gly Gln Asp Cys Thr Ala Cys Asp Leu Thr Cys Pro
 195 200 205
 Met Gly Gln Val Asn Ala Asp Cys Asp Ala Cys Met Cys Gln Asp Phe

210		215		220
Met Leu His Gly Ala Val Ser Leu Pro Gly Gly Ala Pro Ala Ser Gly				
225		230		235
				240
Ala Ala Ile Tyr Leu Leu Thr Lys Thr Pro Lys Leu Leu Thr Gln Thr				
	245		250	255
Asp Ser Asp Gly Arg Phe Arg Ile Pro Gly Leu Cys Pro Asp Gly Lys				
	260		265	270
Ser Ile Leu Lys Ile Thr Lys Val Lys Phe Ala Pro Ile Val Leu Thr				
	275		280	285
Met Pro Lys Thr Ser Leu Lys Ala Ala Thr Ile Lys Ala Glu Phe Val				
	290		295	300
Arg Ala Glu Thr Pro Tyr Met Val Met Asn Pro Glu Thr Lys Ala Arg				
305		310		315
				320
Arg Ala Gly Gln Ser Val Ser Leu Cys Cys Lys Ala Thr Gly Lys Pro				
	325		330	335
Arg Pro Asp Lys Tyr Phe Trp Tyr His Asn Asp Thr Leu Leu Asp Pro				
	340		345	350
Ser Leu Tyr Lys His Glu Ser Lys Leu Val Leu Arg Lys Leu Gln Gln				
	355		360	365
His Gln Ala Gly Glu Tyr Phe Cys Lys Ala Gln Ser Asp Ala Gly Ala				
370		375		380
Val Lys Ser Lys Val Ala Gln Leu Ile Val Thr Ala Ser Asp Glu Thr				
385		390		395
				400
Pro Cys Asn Pro Val Pro Glu Ser Tyr Leu Ile Arg Leu Pro His Asp				
	405		410	415
Cys Phe Gln Asn Ala Thr Asn Ser Phe Tyr Tyr Asp Val Gly Arg Cys				
	420		425	430
Pro Val Lys Thr Cys Ala Gly Gln Gln Asp Asn Gly Ile Arg Cys Arg				
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Asp Ala Val Gln Asn Cys Cys Gly Ile Ser Lys Thr Glu Glu Arg Glu				
450		455		460
Ile Gln Cys Ser Gly Tyr Thr Leu Pro Thr Lys Val Ala Lys Glu Cys				

465		470		475		480
Ser Cys Gln Arg	Cys Thr Glu Thr Arg	Ser Ile Val Arg Gly Arg Val				
	485	490		495		
Ser Ala Ala Asp Asn Gly Glu Pro Met Arg Phe Gly His Val Tyr Met						
	500	505		510		
Gly Asn Ser Arg Val Ser Met Thr Gly Tyr Lys Gly Thr Phe Thr Leu						
	515	520		525		
His Val Pro Gln Asp Thr Glu Arg Leu Val Leu Thr Phe Val Asp Arg						
	530	535		540		
Leu Gln Lys Phe Val Asn Thr Thr Lys Val Leu Pro Phe Asn Lys Lys						
	545	550		555		560
Gly Ser Ala Val Phe His Glu Ile Lys Met Leu Arg Arg Lys Glu Pro						
	565	570		575		
Ile Thr Leu Glu Ala Met Glu Thr Asn Ile Ile Pro Leu Gly Glu Val						
	580	585		590		
Val Gly Glu Asp Pro Met Ala Glu Leu Glu Ile Pro Ser Arg Ser Phe						
	595	600		605		
Tyr Arg Gln Asn Gly Glu Pro Tyr Ile Gly Lys Val Lys Ala Ser Val						
	610	615		620		
Thr Phe Leu Asp Pro Arg Asn Ile Ser Thr Ala Thr Ala Ala Gln Thr						
	625	630		635		640
Asp Leu Asn Phe Ile Asn Asp Glu Gly Asp Thr Phe Pro Leu Arg Thr						
	645	650		655		
Tyr Gly Met Phe Ser Val Asp Phe Arg Asp Glu Val Thr Ser Glu Pro						
	660	665		670		
Leu Asn Ala Gly Lys Val Lys Val His Leu Asp Ser Thr Gln Val Lys						
	675	680		685		
Met Pro Glu His Ile Ser Thr Val Lys Leu Trp Ser Leu Asn Pro Asp						
	690	695		700		
Thr Gly Leu Trp Glu Glu Glu Gly Asp Phe Lys Phe Glu Asn Gln Arg						
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Arg Asn Lys Arg Glu Asp Arg Thr Phe Leu Val Gly Asn Leu Glu Ile						

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Arg Glu Arg Arg Leu Phe Asn Leu Asp Val Pro Glu Ser Arg Arg Cys		
740	745	750
Phe Val Lys Val Arg Ala Tyr Arg Ser Glu Arg Phe Leu Pro Ser Glu		
755	760	765
Gln Ile Gln Gly Val Val Ile Ser Val Ile Asn Leu Glu Pro Arg Thr		
770	775	780
Gly Phe Leu Ser Asn Pro Arg Ala Trp Gly Arg Phe Asp Ser Val Ile		
785	790	800
Thr Gly Pro Asn Gly Ala Cys Val Pro Ala Phe Cys Asp Asp Gln Ser		
805	810	815
Pro Asp Ala Tyr Ser Ala Tyr Val Leu Ala Ser Leu Ala Gly Glu Glu		
820	825	830
Leu Gln Ala Val Glu Ser Ser Pro Lys Phe Asn Pro Asn Ala Ile Gly		
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Val Pro Gln Pro Tyr Leu Asn Lys Leu Asn Tyr Arg Arg Thr Asp His		
850	855	860
Glu Asp Pro Arg Val Lys Lys Thr Ala Phe Gln Ile Ser Met Ala Lys		
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Pro Arg Pro Asn Ser Ala Glu Glu Ser Asn Gly Pro Ile Tyr Ala Phe		
885	890	895
Glu Asn Leu Arg Ala Cys Glu Glu Ala Pro Pro Ser Ala Ala His Phe		
900	905	910
Arg Phe Tyr Gln Ile Glu Gly Asp Arg Tyr Asp Tyr Asn Thr Val Pro		
915	920	925
Phe Asn Glu Asp Asp Pro Met Ser Trp Thr Glu Asp Tyr Leu Ala Trp		
930	935	940
Trp Pro Lys Pro Met Glu Phe Arg Ala Cys Tyr Ile Lys Val Lys Ile		
945	950	955
Val Gly Pro Leu Glu Val Asn Val Arg Ser Arg Asn Met Gly Gly Thr		
965	970	975
His Arg Arg Thr Val Gly Lys Leu Tyr Gly Ile Arg Asp Val Arg Ser		

980	985	990
Thr Arg Asp Arg Asp Gln Pro Asn Val Ser Ala Ala Cys Leu Glu Phe		
995	1000	1005
Lys Cys Ser Gly Met Leu Tyr Asp Gln Asp Arg Val Asp Arg Thr Leu		
1010	1015	1020
Val Lys Val Ile Pro Gln Gly Ser Cys Arg Arg Ala Ser Val Asn Pro		
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Met Leu His Glu Tyr Leu Val Asn His Leu Pro Leu Ala Val Asn Asn		
1045	1050	1055
Asp Thr Ser Glu Tyr Thr Met Leu Ala Pro Leu Asp Pro Leu Gly His		
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Asn Tyr Gly Ile Tyr Thr Val Thr Asp Gln Asp Pro Arg Thr Ala Lys		
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Glu Ile Ala Leu Gly Arg Cys Phe Asp Gly Thr Ser Asp Gly Ser Ser		
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Arg Ile Met Lys Ser Asn Val Gly Val Ala Leu Thr Phe Asn Cys Val		
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Glu Arg Gln Val Gly Arg Gln Ser Ala Phe Gln Tyr Leu Gln Ser Thr		
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Arg Arg Gln Gln Arg Ala Ser Arg Gly Gly Gln Arg Gln Ser Gly Val		
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Leu Phe

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Thr Xaa Lys

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<211> 10

<212> PRT

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Phe Ala Pro Ile Val Leu Asp Met Pro Lys
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<212> PRT

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Asn Pro Ser Ile Phe Ala Lys
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Thr Phe Val Asp Arg Leu Gln Lys
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<223> X AT POSITION 11 INDICATES UNIDENTIFIED RESIDUE

<400> 9

Pro Ala Asp Thr Leu Glu Ser Pro Met Glu Xaa Thr Thr
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<210> 10

<211> 21

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Glu Val Val Gly His
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<210> 11

<211> 16

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<212> PRT

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Leu Val Leu Arg Lys
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Ala Thr Gly Lys Pro Arg Pro Asp Lys
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